High-Resolution Microfluidic Single-Cell Transcriptional Profiling Reveals Clinically Relevant Subtypes among Human Stem Cell Populations Commonly Utilized in Cell-Based Therapies.

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Public Summary:
Stem cell therapies can promote the repair and growth of new neurons, however controversy regarding the best cell source and mechanism of action has slowed progress toward use in human disease, potentially due to differences in the cells that are poorly understood. Single-cell resolution is needed to identify clinically relevant subpopulations with the highest potential for treatments. We have combined single-cell analysis with advanced computational modeling for the first time to study two common sources of cell-based therapies—human neural stem cells and mesenchymal stem cells. This methodology has the potential to inform cell source decisions for any clinical application.

Scientific Abstract:
Stem cell therapies can promote neural repair and regeneration, yet controversy regarding optimal cell source and mechanism of action has slowed clinical translation, potentially due to undefined cellular heterogeneity. Single-cell resolution is needed to identify clinically relevant subpopulations with the highest therapeutic relevance. We combine single-cell microfluidic analysis with advanced computational modeling to study for the first time two common sources for cell-based therapies, human NSCs and MSCs. This methodology has the potential to logically inform cell source decisions for any clinical application.